

SUBSTITUTE SEQUENCE LISTING

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 Rigali, Sebastien
 Dusart, Jean

<120> NUCLEOTIDE AND/OR AMINO-ACID SEQUENCE
 CONTROLLING THE EXPRESSION OF A XYLANASE PROMOTER-OPERATOR
 NUCLEOTIDE SEQUENCE

<130> VANM201.001APC

<140> US 09/762,992

<141> 2001-02-14

<150> PCT/BE99/00105

<151> 1999-08-12

<150> US 60/096,556

<151> 1998-08-14

<160> 9

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 969

<212> DNA

<213> Streptomyces sp. EC3

<220>

<221> CDS

<222> (127)...(936)

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 taggga atg cct gct acc gac gac cgt cgg ccc aag tac cag cgg atc 168
 Met Pro Ala Thr Asp Asp Arg Arg Pro Lys Tyr Gln Arg Ile
 1 5 10

gcg gac tct ttg cga gag gcg atc cag tcg ggc gag tac ggt ccc ggt 216
 Ala Asp Ser Leu Arg Glu Ala Ile Gln Ser Gly Glu Tyr Gly Pro Gly
 15 20 25 30

gat cgg ctt ccc ggg gag aac gac ctc atg gcc acg cac ggc gtg gcc 264
 Asp Arg Leu Pro Gly Glu Asn Asp Leu Met Ala Thr His Gly Val Ala
 35 40 45

cgt atg acg gcc cgg cag gcg ctc ggc gtc ctg cgg gac gag ggc atc 312
 Arg Met Thr Ala Arg Gln Ala Leu Gly Val Leu Arg Asp Glu Gly Ile
 50 55 60

gcc gaa tcc cgg aag ggc gca ggt gtc ttc gtg cgg gcc ttc cgt ccg 360
 Ala Glu Ser Arg Lys Gly Ala Gly Val Phe Val Arg Ala Phe Arg Pro

65	70	75	
ctg cgc cga cgc ggc atc cag cgg ctg gcc cgc gac cag tgg ggc aac			408
Leu Arg Arg Arg Gly Ile Gln Arg Leu Ala Arg Asp Gln Trp Gly Asn			
80	85	90	
gga cgg tcc atc tgg tgc gcg gac atc gag gcc aga gac ctc cgg gtc			456
Gly Arg Ser Ile Trp Ser Ala Asp Ile Glu Ala Arg Asp Leu Arg Val			
95	100	105	110
gac cag gtc tgc gtg ggc gag gag aaa gct ccc gag cac atc ggc gcg			504
Asp Gln Val Ser Val Gly Glu Glu Lys Ala Pro Glu His Ile Gly Ala			
115	120	125	
gtc ctg ggc atg gct gcc gaa gaa gtc gcg tgc gtg agg cgc cgg cgc			552
Val Leu Gly Met Ala Ala Glu Glu Val Ala Cys Val Arg Arg Arg			
130	135	140	
ttc gtc ctg gac ggc aag ccg gtg ctg ctc gcg acg agt tac ctg ccc			600
Phe Val Leu Asp Gly Lys Pro Val Leu Leu Ala Thr Ser Tyr Leu Pro			
145	150	155	
ctg tcc ctg gtg gcc gga tcc gcc atc agc cga gag gac acc ggg ccg			648
Leu Ser Leu Val Ala Gly Ser Ala Ile Ser Arg Glu Asp Thr Gly Pro			
160	165	170	
ggc ggt acc tac gcc cgg ctt gcc gaa ctc ggc cac gaa ccg gtg cac			696
Gly Gly Thr Tyr Ala Arg Leu Ala Glu Leu Gly His Glu Pro Val His			
175	180	185	190
ttc cgc gag gag atc cgc tca cgc atg ccg tgc ccg gac gag gtg aca			744
Phe Arg Glu Glu Ile Arg Ser Arg Met Pro Ser Pro Asp Glu Val Thr			
195	200	205	
cag ctg gac ctt gcc ccg ggc acc ccg gtc atc ctc atc tgc cgc acc			792
Gln Leu Asp Leu Ala Pro Gly Thr Pro Val Ile Leu Ile Cys Arg Thr			
210	215	220	
gcg ttc acc gac cag ggc cac cct gtc gag gtc aac gag atg acc ctg			840
Ala Phe Thr Asp Gln Gly His Pro Val Glu Val Asn Glu Met Thr Leu			
225	230	235	
gac gcc gct tcc tac gtc ttg gag tac gac ttc gac gcg ggc ccc gag			888
Asp Ala Ala Ser Tyr Val Leu Glu Tyr Asp Phe Asp Ala Gly Pro Glu			
240	245	250	
ccc gcc tcc ccc ggc gcc gac gcc aca gcg ccc gga gac ccg gcc tga			936
Pro Ala Ser Pro Gly Ala Asp Ala Thr Ala Pro Gly Asp Pro Ala *			
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<211> 269

<212> PRT

<213> Streptomyces sp. EC3

<400> 2

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Leu Pro Gly Glu Asn Asp Leu Met Ala Thr His Gly Val Ala Arg Met
 35          40          45
Thr Ala Arg Gln Ala Leu Gly Val Leu Arg Asp Glu Gly Ile Ala Glu
 50          55          60
Ser Arg Lys Gly Ala Gly Val Phe Val Arg Ala Phe Arg Pro Leu Arg
 65          70          75          80
Arg Arg Gly Ile Gln Arg Leu Ala Arg Asp Gln Trp Gly Asn Gly Arg
 85          90          95
Ser Ile Trp Ser Ala Asp Ile Glu Ala Arg Asp Leu Arg Val Asp Gln
100          105          110
Val Ser Val Gly Glu Glu Lys Ala Pro Glu His Ile Gly Ala Val Leu
115          120          125
Gly Met Ala Ala Glu Glu Val Ala Cys Val Arg Arg Arg Arg Phe Val
130          135          140
Leu Asp Gly Lys Pro Val Leu Leu Ala Thr Ser Tyr Leu Pro Leu Ser
145          150          155          160
Leu Val Ala Gly Ser Ala Ile Ser Arg Glu Asp Thr Gly Pro Gly Gly
165          170          175
Thr Tyr Ala Arg Leu Ala Glu Leu Gly His Glu Pro Val His Phe Arg
180          185          190
Glu Glu Ile Arg Ser Arg Met Pro Ser Pro Asp Glu Val Thr Gln Leu
195          200          205
Asp Leu Ala Pro Gly Thr Pro Val Ile Leu Ile Cys Arg Thr Ala Phe
210          215          220
Thr Asp Gln Gly His Pro Val Glu Val Asn Glu Met Thr Leu Asp Ala
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Ser Pro Gly Ala Asp Ala Thr Ala Pro Gly Asp Pro Ala
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 <212> DNA
 <213> Streptomyces sp. EC3

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 acggcccggc aggcgctcgg cgtcctgcgg gacgagggca tcgccgaatc ccggaagggc 180
 gcaggtgtct tcgtg 195

<210> 4
 <211> 137
 <212> DNA
 <213> Artificial Sequence

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 <223> polylinker

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cggtaccagg cctaatt 137

<210> 5
 <211> 133
 <212> DNA
 <213> Streptomyces sp. EC3

<400> 5
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 cggtaccagg cct 133

<210> 6
 <211> 12
 <212> DNA
 <213> Streptomyces sp. EC3

<400> 6
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<210> 7
 <211> 16
 <212> DNA
 <213> Streptomyces sp. EC3

<400> 7
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<210> 8
 <211> 12
 <212> DNA
 <213> Streptomyces sp. EC3

<400> 8
 tcgaaacttt cg 12

<210> 9
 <211> 15
 <212> DNA
 <213> Streptomyces sp. EC3

<220>
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 <222> (1)...(15)
 <223> n = A,T,C or G

<400> 9
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